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CORRECTED SEQUENCE LISTING

<110> Conseiller, Emmanuel  
Debussche, Laurent  
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 33

<170> PatentIn version 3.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> oligonucleotide 5'-1(p53)

<400> 1

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<220>  
<221> CDS  
<222> (1)..(885)

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Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

48

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

96

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

144

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca  
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

192

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt  
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

240

aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc  
Page 3

288

Asn	Gln	Gly	Tyr	Glu <sub>85</sub>	Leu	His	Arg	Asp	Gly <sub>90</sub>	Phe	Ser	Cys	Ser	Asp <sub>95</sub>	Ile		
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Asp	Glu	Cys	Gly <sub>100</sub>	Tyr	Ser	Ser	Tyr	Leu <sub>105</sub>	Cys	Gln	Tyr	Arg	Cys <sub>110</sub>	Val	Asn		
gag	cca	ggc	cga	ttc	tcc	tgt	cac	tgc	cca	caa	ggc	tac	cag	ctg	ctg	384	
Glu	Pro	Gly <sub>115</sub>	Arg	Phe	Ser	Cys	His <sub>120</sub>	Cys	Pro	Gln	Gly	Tyr <sub>125</sub>	Gln	Leu	Leu		
gct	aca	agg	ctc	tgc	caa	gat	att	gac	gag	tgt	gaa	aca	ggt	gca	cac	432	
Ala	Thr	Arg	Leu	Cys	Gln	Asp <sub>135</sub>	Ile	Asp	Glu	Cys	Glu <sub>140</sub>	Thr	Gly	Ala	His		
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Gln	Cys	Ser	Glu	Ala	Gln <sub>150</sub>	Thr	Cys	Val	Asn	Phe <sub>155</sub>	His	Gly	Gly	Tyr	Arg <sub>160</sub>		
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Cys	Val	Asp	Thr	Asn <sub>165</sub>	Arg	Cys	Val	Glu	Pro <sub>170</sub>	Tyr	Val	Gln	Val	Ser <sub>175</sub>	Asp		
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Asn	Arg	Cys	Leu <sub>180</sub>	Cys	Pro	Ala	Ser	Asn <sub>185</sub>	Pro	Leu	Cys	Arg	Glu <sub>190</sub>	Gln	Pro		
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Ser	Ser	Ile <sub>195</sub>	Val	His	Arg	Tyr	Met <sub>200</sub>	Ser	Ile	Thr	Ser	Glu <sub>205</sub>	Arg	Ser	Val		
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Pro	Ala	Asp	Val	Phe	Gln	Ile <sub>215</sub>	Gln	Ala	Thr	Ser	Val <sub>220</sub>	Tyr	Pro	Gly	Ala		
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Tyr	Asn	Ala	Phe	Gln	Ile <sub>230</sub>	Arg	Ser	Gly	Asn	Thr <sub>235</sub>	Gln	Gly	Asp	Phe	Tyr <sub>240</sub>		
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Ile	Arg	Gln	Ile	Asn <sub>245</sub>	Asn	Val	Ser	Ala	Met <sub>250</sub>	Leu	Val	Leu	Ala	Arg <sub>255</sub>	Pro		
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Val	Thr	Gly	Pro <sub>260</sub>	Arg	Glu	Tyr	Val	Leu <sub>265</sub>	Asp	Leu	Glu	Met	Val <sub>270</sub>	Thr	Met		
aat	tcc	ctt	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	aga	ctc	acg	gtc	864	
Asn	Ser	Leu <sub>275</sub>	Met	Ser	Tyr	Arg	Ala <sub>280</sub>	Ser	Ser	Val	Leu	Arg <sub>285</sub>	Leu	Thr	Val		
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Phe	Val	Gly	Ala	Tyr	Thr	Phe <sub>295</sub>											
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<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

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20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
Page 5

210

215

220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

Phe Val Gly Ala Tyr Thr Phe  
 290 295

&lt;210&gt; 10

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide c-myc 5'

&lt;400&gt; 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

&lt;210&gt; 11

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; oligonucleotide c-myc 3'

&lt;400&gt; 11

gatctcaggt cctcctcgga gatcagcttc tgctccatg

39

&lt;210&gt; 12

&lt;211&gt; 45

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

<220>  
<223> 5' MCS oligonucleotide

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45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>  
<223> 3' MCS oligonucleotide

<400> 13  
cgcggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>  
<223> oligonucleotide 3' mMBP1

<400> 14  
cgggtactggc agaggtaact gg

22

<210> 15

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<213> Artificial Sequence

<220>  
<223> MBP1 murine (complete sequence)

<220>  
<221> CDS  
<222> (49)..(1377)

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Met Leu Pro  
1

57

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tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His 40 45 50	201
tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly 55 60 65	249
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg 70 75 80	297
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro 85 90 95	345
gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro 100 105 110 115	393
gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu 120 125 130	441
cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr 135 140 145	489
cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val 150 155 160	537
gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn 165 170 175	585
ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly 180 185 190 195	633
cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala 200 205 210	681
cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg 215 220 225	729
tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp 230 235 240	777
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val 245 250 255	825

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ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala 280 285 290	921
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cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr 405 410 415	1305
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gtc ttt gtg gga gcc tat acc ttc tgaagaccct cagggaaggg ccatgtgggg Val Phe Val Gly Ala Tyr Thr Phe 440	1407
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<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

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Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
305 310 315 320

Gln val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

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420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
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<210> 17

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' hMBP1

<400> 17  
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21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5' hMBP1

<400> 18  
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21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

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	tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg	780
	cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga	840
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<211> 684

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

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 tgtctctgcc cggcctccaa ccctctatgt cgagagcagc cttcatccat tgtgcaccgc 300  
 tacatgacca tcacctcgga gcggagcgtg cccgctgacg tggtccagat ccaggcgacc 360  
 tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaactc gcagggggac 420  
 ttttacatta ggcaaataca caacgtcagc gccatgctgg tcctcgcccc gccggtgacg 480  
 ggcccccgga agtacgtgct ggacctggag atggtcacca tgaattccct catgagctac 540  
 cgggccagct ctgtactgag gtcaccgctc ttgttagggg cctacacctt ctgaggagca 600  
 ggagggagcc accctccctg cagctaccct agctgaggag cctgttgtga ggggcagaat 660  
 gagaaaggca ataaaggga aaag 684

<210> 21

<211> 1480

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21  
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ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag Leu Leu Leu Leu Leu Leu Gly Ser Ala 25 Ser Pro Gln Asp Ser 30 Glu Glu	154
ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac Pro Asp Ser Tyr Thr Glu Cys Thr 40 Asp Gly Tyr Glu Trp 45 Asp Pro Asp	202
agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr 60 Ile Pro Glu Ala 50 55 60	250
tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr 75 Gly Gly Tyr Leu Cys 65 70 80	298
ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc Leu Pro Arg Ser Ala Ala Val Ile Asn Asp 90 Leu His Gly Glu Gly Pro 85 90 95	346
ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca ggc Pro Pro Pro Val 100 Pro Pro Ala Gln His 105 Pro Asn Pro Cys Pro Pro Gly 110	394
tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc Tyr Glu Pro 115 Asp Asp Gln Asp Ser 120 Cys Val Asp Val 125 Glu Cys Ala 125	442
cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys 140 His Asn Leu Pro 130 135 140	490
ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc Gly Ser Tyr Gln Cys Thr 150 Cys Pro Asp Gly Tyr 155 Arg Lys Ile Gly Pro 145 150 160	538
gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc Glu Cys Val Asp Ile 165 Asp Glu Cys Arg Tyr 170 Arg Tyr Cys Gln His Arg 165 170 175	586
tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe 180 185 190	634
cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac Gln Leu Gly Pro Asn Asn Arg Ser 200 Cys Val Asp Val 205 Asn Glu Cys Asp 195 200 205	682
atg ggg gcc cca tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe 210 215 220	730
ctg tgt cgc tgc cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His 235 Arg Asp Gly Phe Ser 225 230 240	778
tgc agt gat att gat gag tgt agc tac tcc agc tac ctc tgt cag tac Cys Ser Asp Ile Asp 245 Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr 250 255	826

cgc tgc gtc aac gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt Arg Cys Val Asn 260 Glu Pro Gly Arg Phe 265 Ser Cys His Cys Pro Gln Gly	874
tac cag ctg ctg gcc aca cgc ctc tgc caa gac att gat gag tgt gag Tyr Gln Leu 275 Ala Thr Arg Leu 280 Cys Gln Asp Ile Asp 285 Glu Cys Glu	922
tct ggt gcg cac cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat Ser Gly 290 Ala His Gln Cys Ser 295 Glu Ala Gln Thr Cys 300 Val Asn Phe His	970
ggg ggc tac cgc tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc Gly 305 Gly Tyr Arg Cys Val 310 Asp Thr Asn Arg Cys 315 Val Glu Pro Tyr Ile 320	1018
cag gtc tct gag aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt Gln Val Ser Glu 325 Asn Arg Cys Leu Cys Pro 330 Ala Ser Asn Pro Leu 335 Cys	1066
cga gag cag cct tca tcc att gtg cac cgc tac atg acc atc acc tcg Arg Glu Gln Pro 340 Ser Ser Ile Val His 345 Arg Tyr Met Thr Ile 350 Thr Ser	1114
gag cgg agc gtg ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc Glu Arg Ser Val 355 Pro Ala Asp Val 360 Phe Gln Ile Gln Ala Thr Ser Val	1162
tac ccc ggt gcc tac aat gcc ttt cag atc cgt gct gga aac tcg cag Tyr Pro 370 Gly Ala Tyr Asn Ala 375 Phe Gln Ile Arg Ala 380 Gly Asn Ser Gln	1210
ggg gac ttt tac att agg caa atc aac aac gtc agc gcc atg ctg gtc Gly 385 Asp Phe Tyr Ile Arg 390 Gln Ile Asn Asn Val 395 Ser Ala Met Leu Val 400	1258
ctc gcc cgg ccg gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag Leu Ala Arg Pro 405 Val Thr Gly Pro Arg Glu 410 Tyr Val Leu Asp Leu Glu 415	1306
atg gtc acc atg aat tcc ctc atg agc tac cgg gcc agc tct gta ctg Met Val Thr 420 Met Asn Ser Leu Met Ser Tyr Arg Ala Ser 430 Val Leu	1354
agg ctc acc gtc ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca Arg Leu Thr 435 Val Phe Val Gly Ala Tyr Thr Phe	1407
ccctccctgc agctacccta gctgaggagc ctgtttgtgag gggcagaatg agaaaggcaa	1467
taaagggaga aag	1480

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>  
<223> Human MBP1 (complete sequence)

<400> 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15  
Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30  
Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45  
Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60  
Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80  
Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95  
Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110  
Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125  
Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140  
Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160  
Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175  
Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190  
Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205  
Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
210 215 220  
Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Phe Ala Met Leu Val  
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23  
gctgtggcag aaacccctga cttctgcca ccacctcca gcctcaggat gctccctttt 60  
gcctcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca 120  
gcgtcccccac aggatcccga ggagccggac agctacacgg aatgcacaga tggctatgag 180  
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct 240  
tgcaagggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgctct 300  
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa 360  
caaccaaacc cttgcccga gggctacgag cctgatgaac aggagagctg tgtggatgtg 420  
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttcct 480  
ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggaccgga atgtgtggac 540  
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt 600  
cgatgccagt gtgagccagg cttccagttg ggacctaa accgctcttg tgtggatgtg 660  
aatgagtgtg acatgggagc cccatgtgag cagcgtgct tcaactccta tgggaccttc 720  
ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatc 780  
gatgagtgcg gctactccag ttacctctgc cagtacc 817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cgaggtcaac ggatttggtc gtat

24

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atggtggtga agac

24

<210> 26  
<211> 25  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> antisense-beta-actin oligonucleotide

<400> 26  
cggttgccct tggggttcag ggggg

25

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> sense-MBP1 oligonucleotide

<400> 27  
gccctgatgg ttaccgcaag a

21

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> antisense MBP1 oligonucleotide

<400> 28  
agcccccattg gaagttgaca c

21

<210> 29  
<211> 20  
<212> DNA  
<213> Artificial Sequence  
<220>  
<223> sense-beta-actin oligonucleotide

<400> 29

gtggggcgcc ccaggcacca

20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 30

tgc	acc	tgc	cct	gat	ggt	tac	cgc	aag	atc	ggg	ccc	gag	tgt	gtg	gac	48
Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro	Glu	Cys	Val	Asp	
1				5					10					15		

ata	gac	gag	tgc	cgc	tac	cgc	tac	tgc	cag	cac	cgc	tgc	gtg	aac	ctg	96
Ile	Asp	Glu	Cys	Arg	Tyr	Arg	Tyr	Cys	Gln	His	Arg	Cys	Val	Asn	Leu	
			20					25					30			

cct	ggc	tcc	ttc	cgc	tgc	cag	tgc	gag	ccg	ggc	ttc	cag	ctg	ggg	cct	144
Pro	Gly	Ser	Phe	Arg	Cys	Gln	Cys	Glu	Pro	Gly	Phe	Gln	Leu	Gly	Pro	
		35				40						45				

aac	aac	cgc	tcc	tgt	gtt	gat	gtg	aac	gag	tgt	gac	atg	ggg	gcc	cca	192
Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp	Met	Gly	Ala	Pro	
50						55					60					

tgc	gag	cag	cgc	tgc	ttc	aac	tcc	tat	ggg	acc	ttc	ctg	tgt	cgc	tgc	240
Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	Leu	Cys	Arg	Cys	
65					70				75						80	

cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	tgc	agt	gat	att	288
His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	Cys	Ser	Asp	Ile	
				85					90					95		

gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	cgc	tgc	gtc	aac	336
Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn	
			100					105					110			

gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggt	tac	cag	ctg	ctg	384
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu	
		115					120					125				

gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct	ggt	gcg	cac	432
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ala	His	
130						135					140					

cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg	ggc	tac	cgc	480
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg	
145					150					155					160	

tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag	gtc	tct	gag	528
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu	
				165					170					175		

aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga	gag	cag	cct	576

Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro		
			180					185					190				
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg	624	
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val		
		195					200					205					
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggg	gcc	672	
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala		
	210					215					220						
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac	720	
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr		
225					230					235					240		
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	ccg	768	
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro		
				245					250					255			
gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc	atg	816	
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met		
			260					265					270				
aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	agg	ctc	acc	gtc	864	
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val		
		275					280					285					
ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca	ccctccctgc							915	
Phe	Val	Gly	Ala	Tyr	Thr	Phe											
	290					295											
agctacccta	gctgaggagc	ctgttgtag	gggcagaatg	agaaaggcaa	taaagggaga											975	
aagaaagtcc	tggtggctga	gggtggcg	tcacactgca	ggaagcctca	ggctggggca											1035	
gggtggcact	tggtggggca	ggccaagttc	acctaaatgg	gggtctctat	atgttcaggc											1095	
ccagggggccc	ccattgacag	gagctgggag	ctctgcacca	cgagcttcag	tcaccccag											1155	
aggagaggag	gtaacgagga	gggcggactc	caggcccccg	cccagagatt	tggacttggc											1215	
tggcttgag	gggtcctaag	aaactccact	ctggacagcg	ccaggaggcc	ctgggttcca											1275	
ttcctaactc	tgctcaaac	tgtacattg	gataagccct	agtagttccc	tgggcctggt											1335	
tttctataaaa	acgaggcaac	tgg														1358	

<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

Cys	Thr	Cys	Pro	Asp	Gly	Tyr	Arg	Lys	Ile	Gly	Pro	Glu	Cys	Val	Asp
1				5					10					15	

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
 20 25 30  
 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45  
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60  
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80  
 His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95  
 Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110  
 Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125  
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
 130 135 140  
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160  
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
 165 170 175  
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
 180 185 190  
 Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
 195 200 205  
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
 210 215 220  
 Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
 225 230 235 240  
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255  
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

Phe Val Gly Ala Tyr Thr Phe  
 290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>

<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32

gag	ggc	tct	gaa	tgt	gtg	gat	gtg	aat	gag	tgt	gag	aca	ggt	gtg	cat	48
Glu	Gly	Ser	Glu	Cys	Val	Asp	Val	Asn	Glu	Cys	Glu	Thr	Gly	Val	His	
1				5					10					15		

cgc	tgt	ggc	gag	ggc	caa	ctg	tgc	tat	aac	ctc	cct	gga	tcc	tac	cgc	96
Arg	Cys	Gly	Glu	Gly	Gln	Leu	Cys	Tyr	Asn	Leu	Pro	Gly	Ser	Tyr	Arg	
			20					25					30			

tgt	gac	tgc	aag	ccc	ggc	ttc	cag	agg	gat	gca	ttc	ggc	agg	act	tgc	144
Cys	Asp	Cys	Lys	Pro	Gly	Phe	Gln	Arg	Asp	Ala	Phe	Gly	Arg	Thr	Cys	
		35					40					45				

att	gat	gtg	aac	gaa	tgc	tgg	gtc	tcg	ccg	ggc	cgc	ctg	tgc	cag	cac	192
Ile	Asp	Val	Asn	Glu	Cys	Trp	Val	Ser	Pro	Gly	Arg	Leu	Cys	Gln	His	
50						55				60						

aca	tgt	gag	aac	aca	ccg	ggc	tcc	tac	cgc	tgc	tcc	tgc	gct	gct	ggc	240
Thr	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Tyr	Arg	Cys	Ser	Cys	Ala	Ala	Gly	
65					70				75						80	

ttc	ctt	ttg	gcc	gca	gat	ggc	aaa	cat	tgt	gaa	gat	gtg	aac	gag	tgc	288
Phe	Leu	Leu	Ala	Ala	Asp	Gly	Lys	His	Cys	Glu	Asp	Val	Asn	Glu	Cys	
			85						90					95		

gag	act	cgg	cgc	tgc	agc	cag	gaa	tgt	gcc	aac	atc	tat	ggc	tcc	tat	336
Glu	Thr	Arg	Arg	Cys	Ser	Gln	Glu	Cys	Ala	Asn	Ile	Tyr	Gly	Ser	Tyr	
			100					105					110			

cag	tgc	tac	tgc	cgt	cag	ggc	tac	cag	ctg	gca	gag	gat	ggg	cat	acc	384
Gln	Cys	Tyr	Cys	Arg	Gln	Gly	Tyr	Gln	Leu	Ala	Glu	Asp	Gly	His	Thr	
		115					120					125				

tgc	aca	gac	atc	gat	gag	tgt	gca	cag	ggc	gcg	ggc	att	ctc	tgt	acc	432
Cys	Thr	Asp	Ile	Asp	Glu	Cys	Ala	Gln	Gly	Ala	Gly	Ile	Leu	Cys	Thr	
	130					135					140					

ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu 145 150 155 160	480
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp 165 170 175	528
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His 180 185 190	576
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn 195 200 205	624
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp 210 215 220	672
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu 225 230 235 240	720
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly 245 250 255	768
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys 260 265 270	816
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr 275 280 285	864
ggg gtg gta tcc ctg cag cgg tct gtt ctg gag ccg cgg gac ttt gcc Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala 290 295 300	912
cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe 305 310 315 320	960
ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgaggtgaca Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro 325 330	1009
tgctcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tcctaagtgg	1069
ctttttgctg tgactctgta acttaactta atcatgctga gctggttggt cttgagtctc	1129
taccctagag ggagggagat gcaccccagc aggcactgag tacaggccag ggtcacccga	1189
ggctagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc	1249
aactatggct acagctgaca ttccattcct tcatccactg tgttcctcaa ttaaaaaaaaa	1309
aaatcagctg tgcattgtag cacagacctt taatcctagc actggggagg cagaggtagg	1369
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Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
 65 70 75 80

Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
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Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
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Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
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Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
 130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
 145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
 165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
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Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
325 330

App. No. 09/829,936

Filing Date: April 11, 2001

Inv: Emmanuel CONSEILLER, *et al*

Title: Polypeptide (MBP1) Capable of  
Interacting With Oncogenic Mutants  
of the p53 Protein

Attmy. Ref. No. ST98033

CORRECTED SEQUENCE LISTING

Recorded: May 21, 2003